

## SEQUENCE LISTING

&lt;110&gt; Devgen N.V.

5

Devgen N.V.

<120> Kinase sequences useful for developing compounds for the prevention and/or treatment of metabolic diseases and nucleotide sequences encoding such kinase sequences.

10

&lt;130&gt; P 02-011

15

&lt;160&gt; 13

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

20

&lt;211&gt; 2949

&lt;212&gt; DNA

25

<213> *Caenorhabditis elegans*

&lt;400&gt; 1

atggcgctg ccgtcttaca aaaacccggt gttatcaagg atccatcgat tgctgcattg 60

30

ttcagtaata aggatccaga gcagagatat caagatttaa gagaaattgg acatggatct 120

tttggagctg tctatthttgc atatgacaaa aaaaatgagc agactgttgc gattaaaaag 180

atgaatttta gtggaaaaca ggctgtcgaa aaatggaatg atattcttaa agaagtgtct 240

35

tttctgaata cagttgttca tccacatatt gtcgactaca aggcttgttt tcttaaggac 300

actacatgtt ggcttgtgat ggagtactgt attggctctg cagccgatat agtggatgtc 360

40

ttgcgaaaag gaatgcgaga agtcgaaatc gctgcgattt gctctcaaac tttggatgct 420

cttcgatatc ttcactctct gaagcgaata catcgagata ttaaagctgg aaatattctg 480

45

ctatctgata atgctattgt taaactagct gatttcggat ccgcatccct ggtagatccg 540

gctcaaactt tcatcggaac gccgtttttc atggccccag aggtaattct ggcaatggat 600

gagggtcact acacggatcg tgcagatatt tggtcattgg gtatcacgtg tatagagctg 660

50

gccgaacgtc gtccaccatt gttcagtatg aatgcaatgt ctgccctcta ccatattgct 720

caaaatgata ctccaactct ttctccaatt gacactagcg aacaaccgga atggctcgctg 780

gaattcgttc aatttataga caaatgtctt cgaaaaccag cagaagagcg aatgtcagct 840

55

gaagaatgct ttcgacatcc attcattcaa cggctctcgcc catcagacac aattcaggaa 900

ctcattcaga gaacgaaaaa tatggtatta gagttggata attttcaata caaaaagatg 960  
agaaaactca tgtatttggga tgaaacagaa ggaaaagaag gaagtgaagg aaatggagca 1020  
5 tctgatgatt tagattttca tggaaatgaa gctaattcaa ttggaagagc aggagattct 1080  
gcgtcatctc gaagtgcttc tcttacttct tccgatcaa tgcagagtag tggaggagct 1140  
ggctcttttag tgtccaccaa tacgacgggt gctatggata atgtgcatgg atcctctgga 1200  
10 tacggtaatg gaagtagttc gacgacgagc tccgcacgcc gccgtcctcc aattccttcg 1260  
caaatgctct cttctacatc aacgtctggt gttggaacta tgccgagtca tggatcagtt 1320  
15 ggagcatcga ttacggcgat cgcagtcaat ccaacaccgt ctcttcaga acctatccca 1380  
acatcacaac caacatcgaa atcagaatca tcttctatac tcgaaactgc acacgatgat 1440  
cctttggaca cgtcgatacg tgctccagtg aaagacttgc atatgccgca tcgagcagtc 1500  
20 aaggaacgaa tagccacgtt gcaaaatcac aaattcgca cgcttcgttc ccagagaata 1560  
atcaatcagg aacaagaaga atatacgaaa gagaacaata tgtatgagca aatgagcaag 1620  
25 tacaagcatc tacgacaagc acatcacaaa gagctccaac aatttgaaga acgatgtgca 1680  
ttagatagag agcaactgcg tgtgaaaatg gatcgagaac tcgaacaatt gacaacgaca 1740  
tactcgaaag aaaagatgag agtgaggtgt tcacagaata atgaactaga caaacggaaa 1800  
30 aaagatatcg aagatgggga gaaaaagatg aaaaagacga aaaatagtca aaatcagcag 1860  
cagatgaaac tgtattcagc gcaacaattg aaagaataca agtataacaa ggaggcacag 1920  
35 aaaacacgat tacgaagtct gaacatgcct cgaagtactt atgagaacgc aatgaaagaa 1980  
gtgaaagccg atctgaatcg agtgaaagat gcacgggaaa atgattttga cgagaagctt 2040  
cgtgcagaac ttgaagatga aattgtaagg tatcgcaggc aacaactcag taatcttcat 2100  
40 caattggaag aacaattgga tgatgaagac gtaaacgtgc aagaacgcca aatggacacg 2160  
cgtcacggat tactgtcaaa gcagcatgaa atgacgcgcg atttggaat acagcatctc 2220  
45 aacgagcttc acgcatgaa aaaacgacat ttggagacac aacacgaggc ggaatcggca 2280  
agtcaaatg agtacacaca gaggcaacag gatgaattga gaaaaaagca tgcgatgcag 2340  
tcaagacaac agccaagaga tttaaagatc caagaagcac aaattcgaaa acaataccga 2400  
50 caagttgtga agactcagac tcgccaat ttagctctacc ttacacaaat ggtgcaagta 2460  
gttccaaaag atgaacaaaa agagctcacg tctcgactaa aacaggatca aatgcaaaaa 2520  
55 gtcgcacttc ttgcttcaca atacgaaagt caaatcaaaa aaatggttca ggataagaca 2580  
gtgaagctcg agtcgtggca agaagatgaa caacgggttc ttagtgagaa gttggagaaa 2640

gaattggaag aattgattgc ttatcagaag aagacgagag ccacattaga agagcagatt 2700  
 aaaaaggaac gtacggcact cgaagaacga attggcacac gacgtgcaat gcttgaacag 2760  
 5 aagattattg aagaacgcga acaaattggga gaaatgcgtc gactaaagaa ggagcaaatc 2820  
 cgtgatcgac acagtcaaga acgccatcgt ctcgagaatc atttcgtacg gacgggctcg 2880  
 10 acgagcagaa gttctgggtgg gatcgctcct ggtggtggga attcaagcag tattcagatg 2940  
 gctatgtag 2949

15 <210> 2  
 <211> 982  
 <212> PRT  
 20 <213> *Caenorhabditis elegans*  
 <400> 2

25 Met Ala Pro Ala Val Leu Gln Lys Pro Gly Val Ile Lys Asp Pro Ser  
 1 5 10 15  
 Ile Ala Ala Leu Phe Ser Asn Lys Asp Pro Glu Gln Arg Tyr Gln Asp  
 20 25 30  
 30 Leu Arg Glu Ile Gly His Gly Ser Phe Gly Ala Val Tyr Phe Ala Tyr  
 35 40 45  
 Asp Lys Lys Asn Glu Gln Thr Val Ala Ile Lys Lys Met Asn Phe Ser  
 50 55 60  
 Gly Lys Gln Ala Val Glu Lys Trp Asn Asp Ile Leu Lys Glu Val Ser  
 65 70 75 80  
 40 Phe Leu Asn Thr Val Val His Pro His Ile Val Asp Tyr Lys Ala Cys  
 85 90 95  
 Phe Leu Lys Asp Thr Thr Cys Trp Leu Val Met Glu Tyr Cys Ile Gly  
 100 105 110  
 45 Ser Ala Ala Asp Ile Val Asp Val Leu Arg Lys Gly Met Arg Glu Val  
 115 120 125  
 Glu Ile Ala Ala Ile Cys Ser Gln Thr Leu Asp Ala Leu Arg Tyr Leu  
 130 135 140  
 50 His Ser Leu Lys Arg Ile His Arg Asp Ile Lys Ala Gly Asn Ile Leu  
 145 150 155 160  
 55 Leu Ser Asp His Ala Ile Val Lys Leu Ala Asp Phe Gly Ser Ala Ser  
 165 170 175

	Leu	Val	Asp	Pro	Ala	Gln	Thr	Phe	Ile	Gly	Thr	Pro	Phe	Phe	Met	Ala	
				180					185						190		
5	Pro	Glu	Val	Ile	Leu	Ala	Met	Asp	Glu	Gly	His	Tyr	Thr	Asp	Arg	Ala	
			195					200					205				
	Asp	Ile	Trp	Ser	Leu	Gly	Ile	Thr	Cys	Ile	Glu	Leu	Ala	Glu	Arg	Arg	
		210					215					220					
10	Pro	Pro	Leu	Phe	Ser	Met	Asn	Ala	Met	Ser	Ala	Leu	Tyr	His	Ile	Ala	
		225				230					235					240	
	Gln	Asn	Asp	Pro	Pro	Thr	Leu	Ser	Pro	Ile	Asp	Thr	Ser	Glu	Gln	Pro	
					245					250					255		
15	Glu	Trp	Ser	Leu	Glu	Phe	Val	Gln	Phe	Ile	Asp	Lys	Cys	Leu	Arg	Lys	
				260					265						270		
	Pro	Ala	Glu	Glu	Arg	Met	Ser	Ala	Glu	Glu	Cys	Phe	Arg	His	Pro	Phe	
20			275					280					285				
	Ile	Gln	Arg	Ser	Arg	Pro	Ser	Asp	Thr	Ile	Gln	Glu	Leu	Ile	Gln	Arg	
		290					295					300					
25	Thr	Lys	Asn	Met	Val	Leu	Glu	Leu	Asp	Asn	Phe	Gln	Tyr	Lys	Lys	Met	
		305				310					315					320	
	Arg	Lys	Leu	Met	Tyr	Leu	Asp	Glu	Thr	Glu	Gly	Lys	Glu	Gly	Ser	Glu	
				325						330					335		
30	Gly	Asn	Gly	Ala	Ser	Asp	Asp	Leu	Asp	Phe	His	Gly	Asn	Glu	Ala	Asn	
				340					345					350			
	Ser	Ile	Gly	Arg	Ala	Gly	Asp	Ser	Ala	Ser	Ser	Arg	Ser	Ala	Ser	Leu	
35			355					360					365				
	Thr	Ser	Phe	Arg	Ser	Met	Gln	Ser	Ser	Gly	Gly	Ala	Gly	Leu	Leu	Val	
		370					375					380					
40	Ser	Thr	Asn	Thr	Thr	Gly	Ala	Met	Asp	Asn	Val	His	Gly	Ser	Ser	Gly	
		385				390					395					400	
	Tyr	Gly	Asn	Gly	Ser	Ser	Ser	Thr	Thr	Ser	Ser	Ala	Arg	Arg	Arg	Pro	
					405					410					415		
45	Pro	Ile	Pro	Ser	Gln	Met	Leu	Ser	Ser	Thr	Ser	Thr	Ser	Gly	Val	Gly	
				420					425					430			
	Thr	Met	Pro	Ser	His	Gly	Ser	Val	Gly	Ala	Ser	Ile	Thr	Ala	Ile	Ala	
50			435					440					445				
	Val	Asn	Pro	Thr	Pro	Ser	Pro	Ser	Glu	Pro	Ile	Pro	Thr	Ser	Gln	Pro	
		450					455					460					
55	Thr	Ser	Lys	Ser	Glu	Ser	Ser	Ser	Ile	Leu	Glu	Thr	Ala	His	Asp	Asp	
		465				470					475					480	

	Pro	Leu	Asp	Thr	Ser	Ile	Arg	Ala	Pro	Val	Lys	Asp	Leu	His	Met	Pro	
					.485					490						495	
5	His	Arg	Ala	Val	Lys	Glu	Arg	Ile	Ala	Thr	Leu	Gln	Asn	His	Lys	Phe	
				500					505					510			
	Ala	Thr	Leu	Arg	Ser	Gln	Arg	Ile	Ile	Asn	Gln	Glu	Gln	Glu	Glu	Tyr	
			515					520					525				
10	Thr	Lys	Glu	Asn	Asn	Met	Tyr	Glu	Gln	Met	Ser	Lys	Tyr	Lys	His	Leu	
		530					535					540					
	Arg	Gln	Ala	His	His	Lys	Glu	Leu	Gln	Gln	Phe	Glu	Glu	Arg	Cys	Ala	
	545					550					555					560	
15	Leu	Asp	Arg	Glu	Gln	Leu	Arg	Val	Lys	Met	Asp	Arg	Glu	Leu	Glu	Gln	
					565					570						575	
	Leu	Thr	Thr	Thr	Tyr	Ser	Lys	Glu	Lys	Met	Arg	Val	Arg	Cys	Ser	Gln	
20				580						585				590			
	Asn	Asn	Glu	Leu	Asp	Lys	Arg	Lys	Lys	Asp	Ile	Glu	Asp	Gly	Glu	Lys	
			595					600					605				
25	Lys	Met	Lys	Lys	Thr	Lys	Asn	Ser	Gln	Asn	Gln	Gln	Gln	Met	Lys	Leu	
		610					615					620					
	Tyr	Ser	Ala	Gln	Gln	Leu	Lys	Glu	Tyr	Lys	Tyr	Asn	Lys	Glu	Ala	Gln	
	625					630					635					640	
30	Lys	Thr	Arg	Leu	Arg	Ser	Leu	Asn	Met	Pro	Arg	Ser	Thr	Tyr	Glu	Asn	
					645					650					655		
	Ala	Met	Lys	Glu	Val	Lys	Ala	Asp	Leu	Asn	Arg	Val	Lys	Asp	Ala	Arg	
35				660					665					670			
	Glu	Asn	Asp	Phe	Asp	Glu	Lys	Leu	Arg	Ala	Glu	Leu	Glu	Asp	Glu	Ile	
			675					680					685				
40	Val	Arg	Tyr	Arg	Arg	Gln	Gln	Leu	Ser	Asn	Leu	His	Gln	Leu	Glu	Glu	
		690					695					700					
	Gln	Leu	Asp	Asp	Glu	Asp	Val	Asn	Val	Gln	Glu	Arg	Gln	Met	Asp	Thr	
	705					710					715					720	
45	Arg	His	Gly	Leu	Leu	Ser	Lys	Gln	His	Glu	Met	Thr	Arg	Asp	Leu	Glu	
					725					730					735		
	Ile	Gln	His	Leu	Asn	Glu	Leu	His	Ala	Met	Lys	Lys	Arg	His	Leu	Glu	
50				740					745					750			
	Thr	Gln	His	Glu	Ala	Glu	Ser	Ala	Ser	Gln	Asn	Glu	Tyr	Thr	Gln	Arg	
			755					760					765				
55	Gln	Gln	Asp	Glu	Leu	Arg	Lys	Lys	His	Ala	Met	Gln	Ser	Arg	Gln	Gln	
			770				775					780					

Pro Arg Asp Leu Lys Ile Gln Glu Ala Gln Ile Arg Lys Gln Tyr Arg  
 785 790 795 800  
 5 Gln Val Val Lys Thr Gln Thr Arg Gln Phe Lys Leu Tyr Leu Thr Gln  
 805 810 815  
 Met Val Gln Val Val Pro Lys Asp Glu Gln Lys Glu Leu Thr Ser Arg  
 820 825 830  
 10 Leu Lys Gln Asp Gln Met Gln Lys Val Ala Leu Leu Ala Ser Gln Tyr  
 835 840 845  
 Glu Ser Gln Ile Lys Lys Met Val Gln Asp Lys Thr Val Lys Leu Glu  
 850 855 860  
 15 Ser Trp Gln Glu Asp Glu Gln Arg Val Leu Ser Glu Lys Leu Glu Lys  
 865 870 875 880  
 Glu Leu Glu Glu Leu Ile Ala Tyr Gln Lys Lys Thr Arg Ala Thr Leu  
 885 890 895  
 20 Glu Glu Gln Ile Lys Lys Glu Arg Thr Ala Leu Glu Glu Arg Ile Gly  
 900 905 910  
 25 Thr Arg Arg Ala Met Leu Glu Gln Lys Ile Ile Glu Glu Arg Glu Gln  
 915 920 925  
 Met Gly Glu Met Arg Arg Leu Lys Lys Glu Gln Ile Arg Asp Arg His  
 930 935 940  
 30 Ser Gln Glu Arg His Arg Leu Glu Asn His Phe Val Arg Thr Gly Ser  
 945 950 955 960  
 Thr Ser Arg Ser Ser Gly Gly Ile Ala Pro Gly Val Gly Asn Ser Ser  
 965 970 975  
 35 Ser Ile Gln Met Ala Met  
 980  
 40 <210> 3  
 <211> 4188  
 45 <212> DNA  
 <213> Homo sapiens  
 <300>  
 50 <308> genbank  
 <309> 2002-10-04  
 55 <313> (1)..(4188)

&lt;300&gt;

&lt;308&gt; genbank NM\_016281

5 &lt;309&gt; 2002-10-04

&lt;313&gt; (1) .. (4188)

&lt;400&gt; 3

10 gccggggaac aagccacagg agagcgactc aggaacaagt gtgggagagg aagcggcggc 60  
ggcggcgccg ggcccggggg tggtgacagc aggtctgagg ttgcatcata aatacaaagg 120  
15 actgaagtta taaaagagaa aagagaagtt tgctgctaaa atgaatctga gcaatatgga 180  
atattttgtg ccacacacaa aaagggtactg aagattttacc ccccaaaaaa aattgtcaat 240  
gagaaataaa gctaactgat atcaaaaagc agagcctgct ctactggcca tcatgcgtaa 300  
20 aggggtgctg aaggaccag agattgccga tctattctac aaagatgatc ctgaggaact 360  
ttttattggt ttgcatgaaa ttggacatgg aagttttgga gcagtttatt ttgctacaaa 420  
25 tgctcacacc aatgaggtgg tggcaattaa gaagatgtcc tatagtggga agcagaccca 480  
tgagaaatgg caagatattc ttaaggaagt taaattttta cgacaattga agcatcctaa 540  
tactattgag tacaaaggct gttacttgaa agaacacact gcttggttgg tgatggaata 600  
30 ttgcttaggc tcagcctctg atttattaga agttcataaa aaaccacttc aggaagtgga 660  
gatcgctgcc attactcatg gagccttgca tggactagcc tacctacatt ctcatgcatt 720  
35 gattcatagg gatattaaag caggaaatat tcttctaaca gagccaggtc aggtaaaact 780  
agctgatttt ggatctgctt caatggcttc tcctgccaac tccttcgtgg gcacacctta 840  
ctggatggct ccagaggtga tcttagctat ggatgaagga cagtatgatg ggaaagttga 900  
40 tatttggtca cttggcatca cttgtattga attggcggaa cggaagccgc cccttttcaa 960  
catgaatgca atgagtgcct tatatcacat tgcccagaat gactcccaa cgttacagtc 1020  
45 taatgaatgg acagactcct ttaggagatt tgttgattac tgcttgacaga aaatacctca 1080  
ggaaaggcca acatcagcag aactattaag gcatgacttt gttcgacgag accggccact 1140  
acgtgtcctc attgacctca tacagaggac aaaagatgca gttcgtgagc tagataacct 1200  
50 acagtaccga aaaatgaaaa aaatactttt ccaagagaca cggaatggac ccttgaatga 1260  
gtcacaggag gatgaggaag acagtgaaca tgggaaccagc ctgaacaggg aaatggacag 1320  
55 cctgggcagc aaccattcca ttccaagcat gtccgtgagc acaggcagcc agagcagcag 1380  
tgtgaacagc atgcaggaag tcatggacga gagcagttcc gaacttgtca tgatgcacga 1440

tgacgaaagc acaatcaatt ccagctcctc cgtcgtgcat aagaaagatc atgtattcat 1500  
aagggatgag gcggggccacg gcgatcccag gcctgagccg cggcctaccc agtcagttca 1560  
5 gagccaggcc ctccactacc ggaacagaga gcgctttgcc acgatcaa atcagcatcttt 1620  
ggttacacga cagatccatg agcatgagca ggagaacgag ttgcgggaac agatgtcagg 1680  
10 ttataagcgg atgcggcgcc agcaccagaa gcagctgac gccctggaga acaagctgaa 1740  
ggctgagatg gacgagcacc gcctcaagct acagaaggag gtggagacgc atgccaacaa 1800  
ctcgtccatc gagctggaga agctggccaa gaagcaagtg gctatcatag aaaaggaggc 1860  
15 aaaggtagct gcagcagatg agaagaagtt ccagcaacag atcttggccc agcagaagaa 1920  
agatttgaca actttcttag aaagtcagaa gaagcagtat aagatttgta aggaaaaaat 1980  
20 aaaagaggaa atgaatgagg accatagcac acccaagaaa gagaagcaag agcggatctc 2040  
caaacataaa gagaacttgc agcacacaca ggctgaagag gaagcccacc ttctcactca 2100  
acagagactg tactacgaca aaaattgtcg tttcttcaag cggaaaataa tgatcaagcg 2160  
25 gcacgagggtg gagcagcaga acattcggga ggaactaaat aaaaagagga cccagaagga 2220  
gatggagcat gccatgctaa tccggcacga cgagtccacc cgagagctag agtacaggca 2280  
30 gctgcacacg ttacagaagc tacgcatgga tctgatccgt ttacagcacc agacggaact 2340  
ggaaaaccag ctggagtaca ataagaggcg agaaagagaa ctgcacagaa agcatgtcat 2400  
ggaacttcgg caacagccaa aaaacttaaa ggccatggaa atgcaaatta aaaaacagtt 2460  
35 tcaggacact tgcaaagtac agaccaaaca gtataaagca ctcaagaatc accagttgga 2520  
agttactcca aagaatgagc acaaaaacaat cttaaagaca ctgaaagatg agcagacaag 2580  
40 aaaacttgcc attttggcag agcagtatga acagagtata aatgaaatga tggcctctca 2640  
agcgttacgg ctagatgagg ctcaagaagc agaatgccag gccttgaggc tacagctcca 2700  
gcaggaaatg gagctgctca acgcctacca gagcaaaatc aagatgcaaa cagaggcaca 2760  
45 acatgaacgt gagctccaga agctagagca gagagtgtct ctgcgcagag cacaccttga 2820  
gcagaagatt gaagaggagc tggctgccct tcagaaggaa cgacgcgaga gaataaagaa 2880  
50 cctattggaa aggcaagagc gagagattga aacttttgac atggagagcc tcagaatggg 2940  
atttggaat ttggttacat tagattttcc taaggaggac tacagatgag attaaatttt 3000  
ttgccattta caaaaaaaaaa aaaaaaaga aaacagaaaa aaattcagac cctgcaaaac 3060  
55 cacattcccc attttaacgg gcgttgctct cactctctct ctctcttact cttactgaca 3120



tcgtgtcggg ctagtgcctg tttattctta ctccatcagg ggcccccttc ctccccccgt 3180  
gtcaactttc agtgtctggc aaaacctggc cgtctcttct attcacagta cacgtcacag 3240  
5 tattgatgtg attcaaaatg tttcagtga aactttggag acagttttta caaaaccaat 3300  
aaaccaacaa caaaaaaagt ggatgtatat tgctttaagc aatcactcat taccaccaat 3360  
10 ctgtgaaagt aaagcaaaaa ataataataa taaatgccaa ggggggagaga gacacaatat 3420  
ccgcagcctt acaccttaac tagctgctgc attattttat tttattttat ttttttggtg 3480  
tttattcatc aggaataaaaa aaaacaaagt tttattaaag attgaaaatt tgatacat 3540  
15 tacagaaact aattgtgatg tacatatcag tggtgacata ttattacttt tttggggacg 3600  
ggggtgggtg ggggtgaagag atcttgtgat tttagactgc tgcagagtta acttgtctca 3660  
gcatatctga tgtatcataa tcatttctgc tgtgcagagg agggatacac ttagggggctc 3720  
20 acagatccca gtagcacaat tgggctttgg caaatgggta ttttgtgtat agaggaattt 3780  
aaggagaggt attacttatt ttcataattg attttaactg tttctcggat caaatttttt 3840  
25 aacttcttct tcgtgttctt cccacacctc ttccttttcc agttcagtat ttggagttca 3900  
acactgtctc tcaatcagat catctggatc tttttcttta tctcccttcc ccttcctaag 3960  
tcccatttct tggtcataaa tattgcatta ttcacacttt caaactgtgt attttcttac 4020  
30 aataaaaaat gatgaaaaaa aaaaaggctt tacttctttt gcatgcactt taaaaacaaa 4080  
acaaaacatt tttcaggttc caaggaagag catgataact gtcagagctt ttaattatat 4140  
35 ttgtaaataa aagtgttcat cacaaaaaaa aaaaaaaaaa aaaaaaaaaa 4188

<210> 4

40 <211> 898

<212> PRT

45 <213> Homo sapiens

<300>

50 <308> Genbank NP\_057365.2

<309> 2002-10-01

<313> (1) .. (898)

55

<400> 4

	Met	Arg	Lys	Gly	Val	Leu	Lys	Asp	Pro	Glu	Ile	Ala	Asp	Leu	Phe	Tyr	
	1				5					10					15		
5	Lys	Asp	Asp	Pro	Glu	Glu	Leu	Phe	Ile	Gly	Leu	His	Glu	Ile	Gly	His	
				20					25					30			
	Gly	Ser	Phe	Gly	Ala	Val	Tyr	Phe	Ala	Thr	Asn	Ala	His	Thr	Asn	Glu	
			35					40					45				
10	Val	Val	Ala	Ile	Lys	Lys	Met	Ser	Tyr	Ser	Gly	Lys	Gln	Thr	His	Glu	
		50					55					60					
	Lys	Trp	Gln	Asp	Ile	Leu	Lys	Glu	Val	Lys	Phe	Leu	Arg	Gln	Leu	Lys	
	65					70					75					80	
15	His	Pro	Asn	Thr	Ile	Glu	Tyr	Lys	Gly	Cys	Tyr	Leu	Lys	Glu	His	Thr	
					85					90					95		
	Ala	Trp	Leu	Val	Met	Glu	Tyr	Cys	Leu	Gly	Ser	Ala	Ser	Asp	Leu	Leu	
20				100					105					110			
	Glu	Val	His	Lys	Lys	Pro	Leu	Gln	Glu	Val	Glu	Ile	Ala	Ala	Ile	Thr	
			115					120					125				
25	His	Gly	Ala	Leu	His	Gly	Leu	Ala	Tyr	Leu	His	Ser	His	Ala	Leu	Ile	
		130					135					140					
	His	Arg	Asp	Ile	Lys	Ala	Gly	Asn	Ile	Leu	Leu	Thr	Glu	Pro	Gly	Gln	
	145					150					155					160	
30	Val	Lys	Leu	Ala	Asp	Phe	Gly	Ser	Ala	Ser	Met	Ala	Ser	Pro	Ala	Asn	
					165					170					175		
	Ser	Phe	Val	Gly	Thr	Pro	Tyr	Trp	Met	Ala	Pro	Glu	Val	Ile	Leu	Ala	
35				180					185					190			
	Met	Asp	Glu	Gly	Gln	Tyr	Asp	Gly	Lys	Val	Asp	Ile	Trp	Ser	Leu	Gly	
		195						200					205				
40	Ile	Thr	Cys	Ile	Glu	Leu	Ala	Glu	Arg	Lys	Pro	Pro	Leu	Phe	Asn	Met	
		210					215					220					
	Asn	Ala	Met	Ser	Ala	Leu	Tyr	His	Ile	Ala	Gln	Asn	Asp	Ser	Pro	Thr	
	225					230					235					240	
45	Leu	Gln	Ser	Asn	Glu	Trp	Thr	Asp	Ser	Phe	Arg	Arg	Phe	Val	Asp	Tyr	
					245					250					255		
	Cys	Leu	Gln	Lys	Ile	Pro	Gln	Glu	Arg	Pro	Thr	Ser	Ala	Glu	Leu	Leu	
50				260					265					270			
	Arg	His	Asp	Phe	Val	Arg	Arg	Asp	Arg	Pro	Leu	Arg	Val	Leu	Ile	Asp	
			275					280					285				
55	Leu	Ile	Gln	Arg	Thr	Lys	Asp	Ala	Val	Arg	Glu	Leu	Asp	Asn	Leu	Gln	
		290					295					300					

	Tyr	Arg	Lys	Met	Lys	Lys	Ile	Leu	Phe	Gln	Glu	Thr	Arg	Asn	Gly	Pro	
	305					310					315					320	
5	Leu	Asn	Glu	Ser	Gln	Glu	Asp	Glu	Glu	Asp	Ser	Glu	His	Gly	Thr	Ser	
					325					330					335		
	Leu	Asn	Arg	Glu	Met	Asp	Ser	Leu	Gly	Ser	Asn	His	Ser	Ile	Pro	Ser	
				340					345					350			
10	Met	Ser	Val	Ser	Thr	Gly	Ser	Gln	Ser	Ser	Ser	Val	Asn	Ser	Met	Gln	
			355					360					365				
	Glu	Val	Met	Asp	Glu	Ser	Ser	Ser	Glu	Leu	Val	Met	Met	His	Asp	Asp	
		370					375					380					
15	Glu	Ser	Thr	Ile	Asn	Ser	Ser	Ser	Ser	Val	Val	His	Lys	Lys	Asp	His	
	385					390					395					400	
	Val	Phe	Ile	Arg	Asp	Glu	Ala	Gly	His	Gly	Asp	Pro	Arg	Pro	Glu	Pro	
20					405					410					415		
	Arg	Pro	Thr	Gln	Ser	Val	Gln	Ser	Gln	Ala	Leu	His	Tyr	Arg	Asn	Arg	
				420					425					430			
25	Glu	Arg	Phe	Ala	Thr	Ile	Lys	Ser	Ala	Ser	Leu	Val	Thr	Arg	Gln	Ile	
			435					440					445				
	His	Glu	His	Glu	Gln	Glu	Asn	Glu	Leu	Arg	Glu	Gln	Met	Ser	Gly	Tyr	
		450					455					460					
30	Lys	Arg	Met	Arg	Arg	Gln	His	Gln	Lys	Gln	Leu	Ile	Ala	Leu	Glu	Asn	
	465					470					475					480	
	Lys	Leu	Lys	Ala	Glu	Met	Asp	Glu	His	Arg	Leu	Lys	Leu	Gln	Lys	Glu	
35					485					490					495		
	Val	Glu	Thr	His	Ala	Asn	Asn	Ser	Ser	Ile	Glu	Leu	Glu	Lys	Leu	Ala	
				500					505					510			
40	Lys	Lys	Gln	Val	Ala	Ile	Ile	Glu	Lys	Glu	Ala	Lys	Val	Ala	Ala	Ala	
			515					520					525				
	Asp	Glu	Lys	Lys	Phe	Gln	Gln	Gln	Ile	Leu	Ala	Gln	Gln	Lys	Lys	Asp	
		530					535					540					
45	Leu	Thr	Thr	Phe	Leu	Glu	Ser	Gln	Lys	Lys	Gln	Tyr	Lys	Ile	Cys	Lys	
	545					550					555					560	
	Glu	Lys	Ile	Lys	Glu	Glu	Met	Asn	Glu	Asp	His	Ser	Thr	Pro	Lys	Lys	
50					565					570					575		
	Glu	Lys	Gln	Glu	Arg	Ile	Ser	Lys	His	Lys	Glu	Asn	Leu	Gln	His	Thr	
				580					585					590			
55	Gln	Ala	Glu	Glu	Glu	Ala	His	Leu	Leu	Thr	Gln	Gln	Arg	Leu	Tyr	Tyr	
			595					600					605				



<210> 5  
 <211> 4971  
 5 <212> DNA  
 <213> Homo sapiens  
 10 <300>  
 <308> Genbank NM\_016151.1  
 15 <309> 2002-11-05  
 <313> (1)..(4971)  
 20 <400> 5  
 aattcggcac gagctgagac ggagaagagg agaggcagag agggcgcgagg gaccgtcagc 60  
 agcaccttag ctacaatcgt tcagctattc tcggaagaga gaaggagagag ggaggaggcc 120  
 25 ggggcgggag tgggggctgt caccctcgga ccccggcgtg agaggggccc tgcggccgga 180  
 cgtcctcggg gtggggcccc agtcggtggc cgaagaccta cagctcaggc ccctgggtcc 240  
 caaatttcca ggctttgccc ctctccttt ctcagatacc cgggtaacag tcctcatagt 300  
 30 ccagatatcc gggactcggg tcccaacctc tctaaacctg ggtctctgtt tcatagattt 360  
 tcaaatatca gggttcaggcc cctgcgtgca ccagtatccg ggggttcattc cccgggcgtt 420  
 35 tcaaatatcg gattcagttc ccatcccgtt cagatattcg ggggttcagac cccacaatca 480  
 gaaatccgga attcggcagc tgcgccttc gacgaggggg aggactggac cgcgagggtca 540  
 gattagggttg tcacccctc ccctccaggg gaggttccc gggcccgccc ctcaggaagg 600  
 40 gcgaaagccg aggaagaggt ggcaagggga aaggtctcct tgccccttc cctgcttggc 660  
 agagccgctg gaggaccca ggcggaagcg gaggcgctgg ggcaccatag tgaccctac 720  
 45 caggccaggc cccactctca gggccccag gggccaccat gccagctggg ggccggggccg 780  
 ggagcctgaa ggaccagat gtggctgagc tcttcttcaa ggatgacca gaaaagctct 840  
 tctctgacct ccgggaaatt ggccatggca gctttggagc cgtatacttt gcccgggatg 900  
 50 tccggaatag tgagggtgtg gccatcaaga agatgtccta cagtgggaag cagtccaatg 960  
 agaaatggca agacatcatc aaggagggtgc ggttcttaca gaagctccgg catcccaaca 1020  
 55 ccattcagta ccggggctgt tacctgaggg agcacacggc ttggctggta atggagtatt 1080  
 gcctgggctc agcttctgac cttctagaag tgcacaagaa accccttcag gaggtagaga 1140

	tgcgagctgt	gacccacggg	gcgcttcagg	gcctggcata	tctgcactcc	cacaacatga	1200
	tccatagggga	tgtgaaggct	ggaaacatcc	tgctgtcaga	gccaggggta	gtgaagctag	1260
5	gggacttttg	ttctgcgtcc	atcatggcac	ctgccaaactc	cttcgtgggc	accccatact	1320
	ggatggcacc	cgaggtgatc	ctggccatgg	atgaggggca	gtacgatggc	aaagtggacg	1380
10	tctggctcctt	ggggataacc	tgcatcgagc	tggtgaacg	gaaaccaccg	ctctttaaca	1440
	tgaatgcgat	gagtgcctta	taccacattg	cacagaacga	atccccgtg	ctccagtcag	1500
	gacactggtc	tgagtacttc	cggaattttg	tcgactcctg	tcttcagaaa	atccctcaag	1560
15	acagaccaac	ctcagagggtt	ctcctgaagc	accgctttgt	gctccgggag	cggccaccca	1620
	cagtcatcat	ggacctgatc	cagaggacca	aggatgccgt	gcgggagctg	gacaacctgc	1680
20	agtaccgcaa	gatgaagaag	atcctgttcc	aagaggcacc	caacggccct	ggtgccgagg	1740
	ccccagagga	ggaagaggag	gccgagccct	acatgcaccg	ggccgggact	ctgaccagcc	1800
	tcgagagtag	ccactcagtg	cccagcatgt	ccatcagcgc	ctccagccag	agcagctccg	1860
25	tcaacagcct	agcagatgcc	tcagacaacg	aggaagagga	ggaggaggag	gaggaagagg	1920
	aggaggagga	agaaggccct	gaagcccggg	agatggccat	gatgcaggag	ggggagcaca	1980
30	cagtcacctc	tcacagctcc	attatccacc	ggctgccggg	ctctgacaac	ctatatgatg	2040
	accctacca	gccagagata	acccccagcc	ctctccagcc	gcctgcagcc	ccagctccca	2100
	cttccaccac	ctcttccgcc	cgccgccggg	cctactgccg	taaccgagac	cactttgcca	2160
35	ccatccgaac	cgctccctg	gtcagccgtc	agatccagga	gcatgagcag	gactctgcgc	2220
	tgcgggagca	gctgagcggc	tataagcgga	tgcgacgaca	gcaccagaag	cagctgctgg	2280
40	ccctggagtc	acggctgagg	ggtgaacggg	aggagcacag	tgcacggctg	cagcgggagc	2340
	ttgaggcgca	gcgggctggc	tttggggcag	aggcagaaaa	gctggcccgg	cggcaccagg	2400
	ccataggtga	gaaggaggca	cgagctgcc	aggccgagga	gcggaagttc	cagcagcaca	2460
45	tccttgggca	gcagaagaag	gagctggctg	ccctgctgga	ggcacagaag	cggacctaca	2520
	aacttcgcaa	ggaacagctg	aaggaggagc	tccaggagaa	ccccagcact	cccaagcggg	2580
50	agaaggccga	gtggctgctg	cggcagaagg	agcagctcca	gcagtgccag	gcggaggagg	2640
	aagcagggct	gctgcggcgg	cagcgccagt	actttgagct	gcagtgtcgc	cagtacaagc	2700
	gcaagatggt	gctggctcgg	cacagcctgg	accaggacct	gctgcgggag	gacctgaaca	2760
55	agaagcagac	ccagaaggac	ttggagtgtg	cactgctgct	tcggcagcac	gaggccacgc	2820

	gggagctgga gctgcggcag ctccaggccg tgcagcgcac gcgggctgag ctcacccgcc	2880
	tgcagcacca gacggagctg ggcaaccagc tggagtacaa caagcggcgt gagcaagagt	2940
5	tgcggcagaa gcatgcggcc caggttcgcc agcagcccaa gagcctcaaa gtacgtgcag	3000
	gccagcgcgc cccgggcctt cactcccca ttcttggggc tctgggcca cccaacacag	3060
10	gcacccctat agaacagcag ccctgctcac ctggccagga ggagtcctg gaccaaagaa	3120
	tgcttggcga ggaggaggaa gcagttggag agagaaggat tctgggaaag gaaggggcca	3180
	ctttggagcc caagcagcag aggattctgg gggaagaatc aggagcccct agtcccagtc	3240
15	cacaaaaaca tgggagcctg gttgatgagg aagtttgggg tctgcctgag gagatagagg	3300
	agcttagggg gccctccctt gtaccccagg agaggagcat tgttggccag gaggaggctg	3360
20	ggacgtggag cttgtggggg aaggaggatg agagtcttct ggatgaggag tttgagcttg	3420
	gctgggtcca gggcccagca ctgactcccg tccctgagga ggaggaagaa gaggaagagg	3480
	gggctccgat tgggaccctt agggatcctg gagatggttg tccttcccc gacatccctc	3540
25	ctgaaccccc tccaacacac ctgaggccct gccctgccag ccagctccct ggactcctgt	3600
	cccatggcct cctggccggc ctctcctttg cagtggggtc ctctctggc ctctgcccc	3660
30	tcctgctgct gctgctgctt ccattgctgg cagcccaggg tgggggtggc ctgcaggcag	3720
	cgctgctggc ccttgagggtg gggctgggtg gtctgggggc ctctacctg ctctttgta	3780
	cagccctgca cctgccctcc agtcttttcc tactcctggc ccagggtacc gactggggg	3840
35	ccgtcctggg cctgagctgg cgccgaggcc tcatgggtgt tcccctgggc cttggagctg	3900
	cctggctctt agcttgcca ggcctagctc tacctctggt ggctatggca gcggggggca	3960
40	gatgggtgcg gcagcagggc ccccggtg cccggggcat atctcgactc tggttgcggg	4020
	ttctgctgcg cctgtcacc atggccttcc gggccctgca gggctgtggg gctgtggggg	4080
	accggggtct gtttgactg taccctaaaa ccaacaagga tggcttccgc agccgcctgc	4140
45	ccgtccctgg gcccggcgg cgtaatcccc gcaccacca acaccatta gctctgttgg	4200
	caagggtctg ggtcctgtgc aagggtgga actggcgtct ggcacgggccc agccagggtt	4260
50	tagcatccca cttgcccccg tgggcatcc acacactggc cagctggggc ctgcttcggg	4320
	gtgaacggcc caccgaatc ccccggtac taccacgcag ccagcgccag ctagggcccc	4380
	ctgcctccca ccagccactg ccagggactc tagccgggcg gaggtcacgc acccgccagt	4440
55	ccggggccct gccccctgg aggtagctga ctccagccct tccagcccaa atctagagca	4500
	ttgagcactt tatctccac gactcagtga agtttctcca gtccctagtc ctctcttttc	4560

```

    acccaccttc ctcagtttgc tcacttaccc caggcccagc ccttcggacc tctagacagg 4620
    cagcctcctc agctgtggag tccagcagtc actctgtgtt ctctgggcgc tcctccccta 4680
5   agttattgct gttcgcccgc tgtgtgtgct catcctcacc ctcattgact caggcctggg 4740
    gccagggggtg gtggaggggtg ggaagagtca tgtttttttt ctctcttttg attttgtttt 4800
10  tctgtctccc ttccaacctg tccccttccc cccaccaaaa aaagaaaaag acaaacacaa 4860
    ataaaatata tgagcggaac tgtgaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4920
    aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 4971
15

    <210> 6

    <211> 1235
20  <212> PRT
    <213> Homo sapiens

25  <300>

    <308> Genbank NP_057235.1

30  <309> 2002-11-05
    <313> (1)..(1235)

35  <400> 6

    Met Pro Ala Gly Gly Arg Ala Gly Ser Leu Lys Asp Pro Asp Val Ala
    1          5          10          15
40  Glu Leu Phe Phe Lys Asp Asp Pro Glu Lys Leu Phe Ser Asp Leu Arg
    20          25          30
    Glu Ile Gly His Gly Ser Phe Gly Ala Val Tyr Phe Ala Arg Asp Val
    35          40          45
45  Arg Asn Ser Glu Val Val Ala Ile Lys Lys Met Ser Tyr Ser Gly Lys
    50          55          60
    Gln Ser Asn Glu Lys Trp Gln Asp Ile Ile Lys Glu Val Arg Phe Leu
50  65          70          75          80
    Gln Lys Leu Arg His Pro Asn Thr Ile Gln Tyr Arg Gly Cys Tyr Leu
    85          90          95
55  Arg Glu His Thr Ala Trp Leu Val Met Glu Tyr Cys Leu Gly Ser Ala
    100          105          110

```



	Ser	Asp	Leu	Leu	Glu	Val	His	Lys	Lys	Pro	Leu	Gln	Glu	Val	Glu	Ile	
			115					120					125				
5	Ala	Ala	Val	Thr	His	Gly	Ala	Leu	Gln	Gly	Leu	Ala	Tyr	Leu	His	Ser	
			130				135					140					
	His	Asn	Met	Ile	His	Arg	Asp	Val	Lys	Ala	Gly	Asn	Ile	Leu	Leu	Ser	
	145					150					155					160	
10	Glu	Pro	Gly	Leu	Val	Lys	Leu	Gly	Asp	Phe	Gly	Ser	Ala	Ser	Ile	Met	
					165					170					175		
	Ala	Pro	Ala	Asn	Ser	Phe	Val	Gly	Thr	Pro	Tyr	Trp	Met	Ala	Pro	Glu	
				180					185					190			
15	Val	Ile	Leu	Ala	Met	Asp	Glu	Gly	Gln	Tyr	Asp	Gly	Lys	Val	Asp	Val	
			195					200					205				
	Trp	Ser	Leu	Gly	Ile	Thr	Cys	Ile	Glu	Leu	Ala	Glu	Arg	Lys	Pro	Pro	
20			210				215					220					
	Leu	Phe	Asn	Met	Asn	Ala	Met	Ser	Ala	Leu	Tyr	His	Ile	Ala	Gln	Asn	
	225					230					235					240	
25	Glu	Ser	Pro	Val	Leu	Gln	Ser	Gly	His	Trp	Ser	Glu	Tyr	Phe	Arg	Asn	
					245					250					255		
	Phe	Val	Asp	Ser	Cys	Leu	Gln	Lys	Ile	Pro	Gln	Asp	Arg	Pro	Thr	Ser	
				260					265					270			
30	Glu	Val	Leu	Leu	Lys	His	Arg	Phe	Val	Leu	Arg	Glu	Arg	Pro	Pro	Thr	
			275					280					285				
	Val	Ile	Met	Asp	Leu	Ile	Gln	Arg	Thr	Lys	Asp	Ala	Val	Arg	Glu	Leu	
35			290				295					300					
	Asp	Asn	Leu	Gln	Tyr	Arg	Lys	Met	Lys	Lys	Ile	Leu	Phe	Gln	Glu	Ala	
	305					310					315					320	
40	Pro	Asn	Gly	Pro	Gly	Ala	Glu	Ala	Pro	Glu	Glu	Glu	Glu	Glu	Ala	Glu	
					325					330					335		
	Pro	Tyr	Met	His	Arg	Ala	Gly	Thr	Leu	Thr	Ser	Leu	Glu	Ser	Ser	His	
				340					345					350			
45	Ser	Val	Pro	Ser	Met	Ser	Ile	Ser	Ala	Ser	Ser	Gln	Ser	Ser	Ser	Val	
			355					360					365				
	Asn	Ser	Leu	Ala	Asp	Ala	Ser	Asp	Asn	Glu	Glu	Glu	Glu	Glu	Glu	Glu	
50			370				375					380					
	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	Pro	Glu	Ala	Arg	Glu	Met	Ala	
	385					390					395					400	
55	Met	Met	Gln	Glu	Gly	Glu	His	Thr	Val	Thr	Ser	His	Ser	Ser	Ile	Ile	
					405					410					415		

	His	Arg	Leu	Pro	Gly	Ser	Asp	Asn	Leu	Tyr	Asp	Asp	Pro	Tyr	Gln	Pro	
				420					425					430			
5	Glu	Ile	Thr	Pro	Ser	Pro	Leu	Gln	Pro	Pro	Ala	Ala	Pro	Ala	Pro	Thr	
			435					440					445				
	Ser	Thr	Thr	Ser	Ser	Ala	Arg	Arg	Arg	Ala	Tyr	Cys	Arg	Asn	Arg	Asp	
			450				455					460					
10	His	Phe	Ala	Thr	Ile	Arg	Thr	Ala	Ser	Leu	Val	Ser	Arg	Gln	Ile	Gln	
	465					470					475					480	
	Glu	His	Glu	Gln	Asp	Ser	Ala	Leu	Arg	Glu	Gln	Leu	Ser	Gly	Tyr	Lys	
					485					490					495		
15	Arg	Met	Arg	Arg	Gln	His	Gln	Lys	Gln	Leu	Leu	Ala	Leu	Glu	Ser	Arg	
				500					505					510			
	Leu	Arg	Gly	Glu	Arg	Glu	Glu	His	Ser	Ala	Arg	Leu	Gln	Arg	Glu	Leu	
20			515					520					525				
	Glu	Ala	Gln	Arg	Ala	Gly	Phe	Gly	Ala	Glu	Ala	Glu	Lys	Leu	Ala	Arg	
		530				535						540					
25	Arg	His	Gln	Ala	Ile	Gly	Glu	Lys	Glu	Ala	Arg	Ala	Ala	Gln	Ala	Glu	
	545					550					555					560	
	Glu	Arg	Lys	Phe	Gln	Gln	His	Ile	Leu	Gly	Gln	Gln	Lys	Lys	Glu	Leu	
				565						570					575		
30	Ala	Ala	Leu	Leu	Glu	Ala	Gln	Lys	Arg	Thr	Tyr	Lys	Leu	Arg	Lys	Glu	
			580						585					590			
	Gln	Leu	Lys	Glu	Glu	Leu	Gln	Glu	Asn	Pro	Ser	Thr	Pro	Lys	Arg	Glu	
35			595					600					605				
	Lys	Ala	Glu	Trp	Leu	Leu	Arg	Gln	Lys	Glu	Gln	Leu	Gln	Gln	Cys	Gln	
		610					615					620					
40	Ala	Glu	Glu	Glu	Ala	Gly	Leu	Leu	Arg	Arg	Gln	Arg	Gln	Tyr	Phe	Glu	
	625					630					635					640	
	Leu	Gln	Cys	Arg	Gln	Tyr	Lys	Arg	Lys	Met	Leu	Leu	Ala	Arg	His	Ser	
				645						650					655		
45	Leu	Asp	Gln	Asp	Leu	Leu	Arg	Glu	Asp	Leu	Asn	Lys	Lys	Gln	Thr	Gln	
			660						665					670			
	Lys	Asp	Leu	Glu	Cys	Ala	Leu	Leu	Leu	Arg	Gln	His	Glu	Ala	Thr	Arg	
50			675					680					685				
	Glu	Leu	Glu	Leu	Arg	Gln	Leu	Gln	Ala	Val	Gln	Arg	Thr	Arg	Ala	Glu	
		690					695					700					
55	Leu	Thr	Arg	Leu	Gln	His	Gln	Thr	Glu	Leu	Gly	Asn	Gln	Leu	Glu	Tyr	
	705					710					715					720	

	Asn	Lys	Arg	Arg	Glu	Gln	Glu	Leu	Arg	Gln	Lys	His	Ala	Ala	Gln	Val	
					725					730					735		
5	Arg	Gln	Gln	Pro	Lys	Ser	Leu	Lys	Val	Arg	Ala	Gly	Gln	Arg	Pro	Pro	
				740					745					750			
	Gly	Leu	Pro	Leu	Pro	Ile	Pro	Gly	Ala	Leu	Gly	Pro	Pro	Asn	Thr	Gly	
			755					760					765				
10	Thr	Pro	Ile	Glu	Gln	Gln	Pro	Cys	Ser	Pro	Gly	Gln	Glu	Ala	Val	Leu	
		770					775					780					
	Asp	Gln	Arg	Met	Leu	Gly	Glu	Glu	Glu	Glu	Ala	Val	Gly	Glu	Arg	Arg	
	785					790					795					800	
15	Ile	Leu	Gly	Lys	Glu	Gly	Ala	Thr	Leu	Glu	Pro	Lys	Gln	Gln	Arg	Ile	
					805					810					815		
	Leu	Gly	Glu	Glu	Ser	Gly	Ala	Pro	Ser	Pro	Ser	Pro	Gln	Lys	His	Gly	
20					820				825					830			
	Ser	Leu	Val	Asp	Glu	Glu	Val	Trp	Gly	Leu	Pro	Glu	Glu	Ile	Glu	Glu	
			835					840					845				
25	Leu	Arg	Val	Pro	Ser	Leu	Val	Pro	Gln	Glu	Arg	Ser	Ile	Val	Gly	Gln	
		850					855					860					
	Glu	Glu	Ala	Gly	Thr	Trp	Ser	Leu	Trp	Gly	Lys	Glu	Asp	Glu	Ser	Leu	
	865					870					875					880	
30	Leu	Asp	Glu	Glu	Phe	Glu	Leu	Gly	Trp	Val	Gln	Gly	Pro	Ala	Leu	Thr	
					885					890					895		
	Pro	Val	Pro	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	Ala	Pro	Ile	Gly	
35				900					905					910			
	Thr	Pro	Arg	Asp	Pro	Gly	Asp	Gly	Cys	Pro	Ser	Pro	Asp	Ile	Pro	Pro	
			915					920					925				
40	Glu	Pro	Pro	Pro	Thr	His	Leu	Arg	Pro	Cys	Pro	Ala	Ser	Gln	Leu	Pro	
		930					935					940					
	Gly	Leu	Leu	Ser	His	Gly	Leu	Leu	Ala	Gly	Leu	Ser	Phe	Ala	Val	Gly	
	945					950					955					960	
45	Ser	Ser	Ser	Gly	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Leu	
					965					970					975		
	Leu	Ala	Ala	Gln	Gly	Gly	Gly	Gly	Leu	Gln	Ala	Ala	Leu	Leu	Ala	Leu	
50				980					985					990			
	Glu	Val	Gly	Leu	Val	Gly	Leu	Gly	Ala	Ser	Tyr	Leu	Leu	Leu	Cys	Thr	
			995					1000					1005				
55	Ala	Leu	His	Leu	Pro	Ser	Ser	Leu	Phe	Leu	Leu	Leu	Ala	Gln	Gly		
		1010					1015						1020				

	Thr Ala	Leu Gly	Ala Val	Leu	Gly Leu	Ser Trp	Arg	Arg Gly	Leu
	1025			1030			1035		
5	Met Gly	Val Pro	Leu Gly	Leu	Gly Ala	Ala Trp	Leu	Leu Ala	Trp
	1040			1045			1050		
	Pro Gly	Leu Ala	Leu Pro	Leu	Val Ala	Met Ala	Ala	Gly Gly	Arg
	1055			1060			1065		
10	Trp Val	Arg Gln	Gln Gly	Pro	Arg Val	Arg Arg	Gly	Ile Ser	Arg
	1070			1075			1080		
	Leu Trp	Leu Arg	Val Leu	Leu	Arg Leu	Ser Pro	Met	Ala Phe	Arg
	1085			1090			1095		
15	Ala Leu	Gln Gly	Cys Gly	Ala	Val Gly	Asp Arg	Gly	Leu Phe	Ala
	1100			1105			1110		
	Leu Tyr	Pro Lys	Thr Asn	Lys	Asp Gly	Phe Arg	Ser	Arg Leu	Pro
20	1115			1120			1125		
	Val Pro	Gly Pro	Arg Arg	Arg	Asn Pro	Arg Thr	Thr	Gln His	Pro
	1130			1135			1140		
25	Leu Ala	Leu Leu	Ala Arg	Val	Trp Val	Leu Cys	Lys	Gly Trp	Asn
	1145			1150			1155		
	Trp Arg	Leu Ala	Arg Ala	Ser	Gln Gly	Leu Ala	Ser	His Leu	Pro
	1160			1165			1170		
30	Pro Trp	Ala Ile	His Thr	Leu	Ala Ser	Trp Gly	Leu	Leu Arg	Gly
	1175			1180			1185		
	Glu Arg	Pro Thr	Arg Ile	Pro	Arg Leu	Leu Pro	Arg	Ser Gln	Arg
35	1190			1195			1200		
	Gln Leu	Gly Pro	Pro Ala	Ser	His Gln	Pro Leu	Pro	Gly Thr	Leu
	1205			1210			1215		
40	Ala Gly	Arg Arg	Ser Arg	Thr	Arg Gln	Ser Arg	Ala	Leu Pro	Pro
	1220			1225			1230		
	Trp Arg								
	1235								
45									
	<210>	7							
	<211>	4242							
50	<212>	DNA							
	<213>	Homo sapiens							
55	<300>								

<308> Genbank NM\_004783

<309> 2000-11-01

5 <313> (1)..(4242)

<400> 7

10	agaatttcaa atatcagggt caggccccctg cgtgcaccag tatccggggt tcattccccg	60
	ggcgttcaaa tatcggattc agtctccatc ccgttcagat attcgggggt cagacccccac	120
	aatcagaaat ccggaattcg gcagctgtcg ccctcgacga gggggaggac tggaccgcga	180
15	ggtcagatta gggtgtcacc ccctccccctc caggggaggc ttcccggggc cgccccctcag	240
	gaagggcgaa agccgaggaa gaggtggcaa ggggaaaggc ctccctgccc ctctccctgc	300
	ttggcagagc cgctggagga cccagggcgg aagcggaggc gctggggcac catagtgacc	360
20	cctaccaggc caggccccac tctcagggcc ccagggggcc accatgccag ctggggggccg	420
	ggccgggagc ctgaaggacc cagatgtggc tgagctcttc ttcaaggatg acccagaaaa	480
25	gctcttctct gacctccggg aaattggcca tggcagcttt ggagccgtat actttgcccg	540
	ggatgtccgg aatagtgagg tgggtggcat caagaagatg tcctacagtg ggaagcagtc	600
	caatgagaaa tggcaagaca tcatcaagga ggtgcggttc ttacagaagc tccggcatcc	660
30	caacaccatt cagtaccggg gctgttacct gagggagcac acggcttggc tggtaatgga	720
	gtattgcctg ggctcagctt ctgaccttct agaagtgcac aagaaacccc ttcaggaggt	780
35	agagatcgca gctgtgaccc acggggcgct tcagggcctg gcatatctgc actcccacaa	840
	catgatccat agggatgtga aggctggaaa catcctgctg tcagagccag ggtagtgaa	900
	gctaggggac tttgggtctg cgtccatcat ggcacctgcc aactccttcg tgggcacccc	960
40	atactggatg gcacccgagg tgatcctggc catggatgag gggcagtacg atggcaaagt	1020
	ggacgtctgg tccttgggga taacctgcat cgagctggct gaacggaaac caccgtcttt	1080
45	taacatgaat gcgatgagt ccttatacca cattgcacag aacgaatccc ccgtgctcca	1140
	gtcaggacac tgggtctgagt acttccggaa ttttgtcgac tcctgtcttc agaaaatccc	1200
	tcaagacaga ccaacctcag aggttctcct gaagcaccgc tttgtgctcc gggagcggcc	1260
50	accacagtc atcatggacc tgatccagag gaccaaggat gccgtgcggg agctggacaa	1320
	cctgcagtac cgcaagatga agaagatcct gttccaagag gcaccaacg gccctggtgc	1380
55	cgaggcccca gaggaggaag aggaggccga gccctacatg caccgggccc ggactctgac	1440
	cagcctcgag agtagccact cagtgccag catgtccatc agcgcctcca gccagagcag	1500

	ctccgtcaac agcctagcag atgcctcaga caacgaggaa gaggaggagg aggaggagga	1560
5	agaggaggag gaggaagaag gccctgaagc ccgggagatg gccatgatgc aggaggggga	1620
	gcacacagtc acctctcaca gctccattat ccaccggctg ccgggctctg acaacctata	1680
	tgatgacccc taccagccag agataacccc cagccctctc cagccgcctg cagccccagc	1740
10	tccccacttcc accacctctt ctgcccgcgc ccggggcctac tgccgtaacc gagaccactt	1800
	tgccaccatc cgaaccgcct ccctggtcag ccgtcagatc caggagcatg agcaggactc	1860
15	tgcgctgcgg gagcagctga gcggctataa gcggatgcga cgacagcacc agaagcagct	1920
	gctggccctg gagtcacggc tgaggggtga acgggaggag cacagtgcac ggctgcagcg	1980
	ggagcttgag gcgcagcggg ctggctttgg ggcagaggca gaaaagctgg cccggcggca	2040
20	ccaggccata ggtgagaagg aggcacgagc tgcccaggcc gaggagcggg agttccagca	2100
	gcacatcctt gggcagcaga agaaggagct ggctgccctg ctggaggcac agaagcggac	2160
25	ctacaaaactt cgcaaggaac agctgaagga ggagctccag gagaacccca gcaactccaa	2220
	gcggggagaag gccgagtggc tgctgcggca gaaggagcag ctccagcagt gccaggcggg	2280
	ggaggaagca gggctgctgc ggcggcagcg ccagtacttt gagctgcagt gtcgccagta	2340
30	caagcgcaag atgttgctgg ctcggcacag cctggaccag gacctgctgc gggaggacct	2400
	gaacaagaag cagaccacaga aggacttggg gtgtgcactg ctgcttcggc agcacgaggc	2460
35	cacgcgggag ctggagctgc ggcagctcca ggccgtgcag cgcacgcggg ctgagctcac	2520
	ccgcctgcag caccagacgg agctgggcaa ccagctggag tacaacaagc ggcgtgagca	2580
	agagttgcgg cagaagcatg cggcccaggt tcgccagcag cccaagagcc tcaaacttaa	2640
40	ggagctgcag atcaagaagc agttccagga gacgtgtaag atccagactc ggcagtacaa	2700
	ggctctgcga gcacacttgc tggagaccac gccc aaagct cagcacaaga gcctccttaa	2760
45	gcggctcaag gaagagcaga cccgcaagct ggcgatcttg gcggagcagt atgaccagtc	2820
	catctcagag atgctcagct cacaggcgct gcggcttgat gagacccagg aggcagagtt	2880
	ccaggccctt cggcagcagc ttcaacagga gctggagctg ctcaacgctt accagagcaa	2940
50	gatcaagatc cgcacagaga gccagcacga gagggagctg cgggagctgg agcagagggg	3000
	cgcgctgcgg cgggcactgc tggagcagcg ggtggaagag gagctgctgg ccctgcagac	3060
55	aggacgctcc gagcgaatcc gcagtctgct tgagcggcag gcccgtaga tcgaggcctt	3120
	cgatgcggaa agcatgaggc tgggcttctc cagcatggct ctgggggggca tcccggctga	3180

agctgctgcc cagggctatc ctgctccacc ccctgccccca gcctggccct cccgtcccgt 3240  
tccccgttct ggggcacact ggagccatgg ccctcctcca ccaggcatgc cccctccagc 3300  
5 ctggcgctcag ccgtctctgc tggctcccc aggcccccca aactggctgg ggccccccac 3360  
acaaagtggg acaccccgctg gcggagccct gctgctgcta agaaacagcc cccagcccct 3420  
10 gcggcgggca gcctcggggg gcagtggcag tgagaatgtg ggccccctg ctgccgcggt 3480  
gcccggggcc ctgagccgca gcaccagtgt cgcttccca atcctcaatg gttcttccca 3540  
cttctattcc tgaggtgcag cggggaggag cagatgagct gggcagggca ggggtgggtg 3600  
15 gagcctgacc ctggagggca ctgagctgga ggcccctgca agggtagggg acaagatgta 3660  
ggctccagct cccctcagac ctctcatct catgagcttc ttggggctgg ccagtggccc 3720  
agggccagct tggcgataga tgcctcaagg ctgcctggga gcccgcctc cctaccatgg 3780  
20 tgccaggggt ctccctccgc cacctaggaa aggagggaga tgtgcgtgtc aaatattcat 3840  
ctagtccctt gggggagggg aagggtgggt ctagacatac tatattcaga gaactatact 3900  
25 accctcacag tgaggccctc agacctgcca cagggcagag caggtctggg gcctgaggca 3960  
gggagaatga gaggccacct tactggcagg aaggatcagg atggggctctt ggggtcagga 4020  
tgctgggtc tcttcccgta actgtctgac gtcctgtgcc gtcttgtcct ttatcttttt 4080  
30 tttttttttt taattgggat cagggtctggg gcggggaaac aagggaagga ccttggaagg 4140  
ggctgctccc aggcctgggg ggcagctcgt ggagcccctc tcagctgtgg ggctggcaca 4200  
35 gagccccagg caagctttta ataaactgtt gggtatttcta ac 4242

<210> 8

40 <211> 1049

<212> PRT

45 <213> Homo sapiens

<300>

50 <308> Genbank NP\_004774.1

<309> 2000-11-01

<313> (1) .. (1049)

55

<400> 8

	Met	Pro	Ala	Gly	Gly	Arg	Ala	Gly	Ser	Leu	Lys	Asp	Pro	Asp	Val	Ala	
	1				5					10					15		
5	Glu	Leu	Phe	Phe	Lys	Asp	Asp	Pro	Glu	Lys	Leu	Phe	Ser	Asp	Leu	Arg	
				20					25					30			
	Glu	Ile	Gly	His	Gly	Ser	Phe	Gly	Ala	Val	Tyr	Phe	Ala	Arg	Asp	Val	
			35					40					45				
10	Arg	Asn	Ser	Glu	Val	Val	Ala	Ile	Lys	Lys	Met	Ser	Tyr	Ser	Gly	Lys	
		50					55					60					
	Gln	Ser	Asn	Glu	Lys	Trp	Gln	Asp	Ile	Ile	Lys	Glu	Val	Arg	Phe	Leu	
	65					70					75					80	
15	Gln	Lys	Leu	Arg	His	Pro	Asn	Thr	Ile	Gln	Tyr	Arg	Gly	Cys	Tyr	Leu	
					85					90					95		
	Arg	Glu	His	Thr	Ala	Trp	Leu	Val	Met	Glu	Tyr	Cys	Leu	Gly	Ser	Ala	
20				100					105					110			
	Ser	Asp	Leu	Leu	Glu	Val	His	Lys	Lys	Pro	Leu	Gln	Glu	Val	Glu	Ile	
			115					120					125				
25	Ala	Ala	Val	Thr	His	Gly	Ala	Leu	Gln	Gly	Leu	Ala	Tyr	Leu	His	Ser	
		130					135					140					
	His	Asn	Met	Ile	His	Arg	Asp	Val	Lys	Ala	Gly	Asn	Ile	Leu	Leu	Ser	
	145					150					155					160	
30	Glu	Pro	Gly	Leu	Val	Lys	Leu	Gly	Asp	Phe	Gly	Ser	Ala	Ser	Ile	Met	
				165						170					175		
	Ala	Pro	Ala	Asn	Ser	Phe	Val	Gly	Thr	Pro	Tyr	Trp	Met	Ala	Pro	Glu	
35				180					185					190			
	Val	Ile	Leu	Ala	Met	Asp	Glu	Gly	Gln	Tyr	Asp	Gly	Lys	Val	Asp	Val	
			195					200					205				
40	Trp	Ser	Leu	Gly	Ile	Thr	Cys	Ile	Glu	Leu	Ala	Glu	Arg	Lys	Pro	Pro	
		210					215					220					
	Leu	Phe	Asn	Met	Asn	Ala	Met	Ser	Ala	Leu	Tyr	His	Ile	Ala	Gln	Asn	
	225					230					235					240	
45	Glu	Ser	Pro	Val	Leu	Gln	Ser	Gly	His	Trp	Ser	Glu	Tyr	Phe	Arg	Asn	
				245						250					255		
	Phe	Val	Asp	Ser	Cys	Leu	Gln	Lys	Ile	Pro	Gln	Asp	Arg	Pro	Thr	Ser	
50				260					265					270			
	Glu	Val	Leu	Leu	Lys	His	Arg	Phe	Val	Leu	Arg	Glu	Arg	Pro	Pro	Thr	
			275					280					285				
55	Val	Ile	Met	Asp	Leu	Ile	Gln	Arg	Thr	Lys	Asp	Ala	Val	Arg	Glu	Leu	
		290					295					300					



	Asp	Asn	Leu	Gln	Tyr	Arg	Lys	Met	Lys	Lys	Ile	Leu	Phe	Gln	Glu	Ala	
	305					310					315					320	
5	Pro	Asn	Gly	Pro	Gly	Ala	Glu	Ala	Pro	Glu	Glu	Glu	Glu	Glu	Ala	Glu	
					325					330					335		
	Pro	Tyr	Met	His	Arg	Ala	Gly	Thr	Leu	Thr	Ser	Leu	Glu	Ser	Ser	His	
				340					345					350			
10	Ser	Val	Pro	Ser	Met	Ser	Ile	Ser	Ala	Ser	Ser	Gln	Ser	Ser	Ser	Val	
			355					360					365				
	Asn	Ser	Leu	Ala	Asp	Ala	Ser	Asp	Asn	Glu	Glu	Glu	Glu	Glu	Glu	Glu	
15		370					375					380					
	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	Pro	Glu	Ala	Arg	Glu	Met	Ala	
	385					390					395					400	
20	Met	Met	Gln	Glu	Gly	Glu	His	Thr	Val	Thr	Ser	His	Ser	Ser	Ile	Ile	
					405					410					415		
	His	Arg	Leu	Pro	Gly	Ser	Asp	Asn	Leu	Tyr	Asp	Asp	Pro	Tyr	Gln	Pro	
				420					425					430			
25	Glu	Ile	Thr	Pro	Ser	Pro	Leu	Gln	Pro	Pro	Ala	Ala	Pro	Ala	Pro	Thr	
			435					440					445				
	Ser	Thr	Thr	Ser	Ser	Ala	Arg	Arg	Arg	Ala	Tyr	Cys	Arg	Asn	Arg	Asp	
30		450					455					460					
	His	Phe	Ala	Thr	Ile	Arg	Thr	Ala	Ser	Leu	Val	Ser	Arg	Gln	Ile	Gln	
	465					470					475					480	
35	Glu	His	Glu	Gln	Asp	Ser	Ala	Leu	Arg	Glu	Gln	Leu	Ser	Gly	Tyr	Lys	
					485					490					495		
	Arg	Met	Arg	Arg	Gln	His	Gln	Lys	Gln	Leu	Leu	Ala	Leu	Glu	Ser	Arg	
				500					505					510			
40	Leu	Arg	Gly	Glu	Arg	Glu	Glu	His	Ser	Ala	Arg	Leu	Gln	Arg	Glu	Leu	
			515					520					525				
	Glu	Ala	Gln	Arg	Ala	Gly	Phe	Gly	Ala	Glu	Ala	Glu	Lys	Leu	Ala	Arg	
45		530					535					540					
	Arg	His	Gln	Ala	Ile	Gly	Glu	Lys	Glu	Ala	Arg	Ala	Ala	Gln	Ala	Glu	
	545					550					555					560	
50	Glu	Arg	Lys	Phe	Gln	Gln	His	Ile	Leu	Gly	Gln	Gln	Lys	Lys	Glu	Leu	
					565					570					575		
	Ala	Ala	Leu	Leu	Glu	Ala	Gln	Lys	Arg	Thr	Tyr	Lys	Leu	Arg	Lys	Glu	
				580					585					590			
55	Gln	Leu	Lys	Glu	Glu	Leu	Gln	Glu	Asn	Pro	Ser	Thr	Pro	Lys	Arg	Glu	
			595					600					605				

	Lys	Ala	Glu	Trp	Leu	Leu	Arg	Gln	Lys	Glu	Gln	Leu	Gln	Gln	Cys	Gln	
	610						615					620					
5	Ala	Glu	Glu	Glu	Ala	Gly	Leu	Leu	Arg	Arg	Gln	Arg	Gln	Tyr	Phe	Glu	
	625					630					635					640	
	Leu	Gln	Cys	Arg	Gln	Tyr	Lys	Arg	Lys	Met	Leu	Leu	Ala	Arg	His	Ser	
					645					650					655		
10	Leu	Asp	Gln	Asp	Leu	Leu	Arg	Glu	Asp	Leu	Asn	Lys	Lys	Gln	Thr	Gln	
				660					665					670			
	Lys	Asp	Leu	Glu	Cys	Ala	Leu	Leu	Leu	Arg	Gln	His	Glu	Ala	Thr	Arg	
			675					680					685				
15	Glu	Leu	Glu	Leu	Arg	Gln	Leu	Gln	Ala	Val	Gln	Arg	Thr	Arg	Ala	Glu	
		690					695					700					
	Leu	Thr	Arg	Leu	Gln	His	Gln	Thr	Glu	Leu	Gly	Asn	Gln	Leu	Glu	Tyr	
20		705				710					715					720	
	Asn	Lys	Arg	Arg	Glu	Gln	Glu	Leu	Arg	Gln	Lys	His	Ala	Ala	Gln	Val	
					725					730					735		
25	Arg	Gln	Gln	Pro	Lys	Ser	Leu	Lys	Ser	Lys	Glu	Leu	Gln	Ile	Lys	Lys	
				740					745					750			
	Gln	Phe	Gln	Glu	Thr	Cys	Lys	Ile	Gln	Thr	Arg	Gln	Tyr	Lys	Ala	Leu	
			755					760					765				
30	Arg	Ala	His	Leu	Leu	Glu	Thr	Thr	Pro	Lys	Ala	Gln	His	Lys	Ser	Leu	
		770					775					780					
	Leu	Lys	Arg	Leu	Lys	Glu	Glu	Gln	Thr	Arg	Lys	Leu	Ala	Ile	Leu	Ala	
35		785				790				795						800	
	Glu	Gln	Tyr	Asp	Gln	Ser	Ile	Ser	Glu	Met	Leu	Ser	Ser	Gln	Ala	Leu	
				805					810						815		
40	Arg	Leu	Asp	Glu	Thr	Gln	Glu	Ala	Glu	Phe	Gln	Ala	Leu	Arg	Gln	Gln	
				820					825					830			
	Leu	Gln	Gln	Glu	Leu	Glu	Leu	Leu	Asn	Ala	Tyr	Gln	Ser	Lys	Ile	Lys	
			835				840						845				
45	Ile	Arg	Thr	Glu	Ser	Gln	His	Glu	Arg	Glu	Leu	Arg	Glu	Leu	Glu	Gln	
		850					855					860					
	Arg	Val	Ala	Leu	Arg	Arg	Ala	Leu	Leu	Glu	Gln	Arg	Val	Glu	Glu	Glu	
50		865				870					875					880	
	Leu	Leu	Ala	Leu	Gln	Thr	Gly	Arg	Ser	Glu	Arg	Ile	Arg	Ser	Leu	Leu	
				885					890						895		
55	Glu	Arg	Gln	Ala	Arg	Glu	Ile	Glu	Ala	Phe	Asp	Ala	Glu	Ser	Met	Arg	
			900						905					910			

Leu Gly Phe Ser Ser Met Ala Leu Gly Gly Ile Pro Ala Glu Ala Ala  
915 920 925

5 Ala Gln Gly Tyr Pro Ala Pro Pro Pro Ala Pro Ala Trp Pro Ser Arg  
930 935 940

Pro Val Pro Arg Ser Gly Ala His Trp Ser His Gly Pro Pro Pro Pro  
945 950 955 960

10 Gly Met Pro Pro Pro Ala Trp Arg Gln Pro Ser Leu Leu Ala Pro Pro  
965 970 975

Gly Pro Pro Asn Trp Leu Gly Pro Pro Thr Gln Ser Gly Thr Pro Arg  
980 985 990

15 Gly Gly Ala Leu Leu Leu Leu Arg Asn Ser Pro Gln Pro Leu Arg Arg  
995 1000 1005

20 Ala Ala Ser Gly Gly Ser Gly Ser Glu Asn Val Gly Pro Pro Ala  
1010 1015 1020

Ala Ala Val Pro Gly Pro Leu Ser Arg Ser Thr Ser Val Ala Ser  
1025 1030 1035

25 His Ile Leu Asn Gly Ser Ser His Phe Tyr Ser  
1040 1045

<210> 9

30 <211> 3285

<212> DNA

35 <213> Homo sapiens

<220>

40 <221> misc\_feature

<222> (3245)..(3245)

<223> a, t, c or g

45 <220>

<221> misc\_feature

50 <222> (3263)..(3263)

<223> a, t, c or g

55 <220>

<221> misc\_feature  
 <222> (3278)..(3278)  
 5 <223> a, t, c or g  
  
 <220>  
 10 <221> misc\_feature  
 <222> (72)..(72)  
 <223> a, t, c or g  
 15  
 <300>  
 <308> EMBL AY049015  
 20 <309> 2001-10-15  
 <313> (1)..(3285)  
 25  
 <400> 9  
 caacggattt catttcatac agatgaacca aggatcggga tagcagtata aaattagaat 60  
 caagacagct gntcgccaag caggatgcc a tcaactaaca gagcaggcag cctgaaggac 120  
 30 cctgaaattg cagagctctt cttcaaagaa gatccagaga agctcttcac agatctcaga 180  
 gaaattggcc atggaagctt tggagcagtg tattttgcac gagatgtgcg taccaatgaa 240  
 35 gtggtggcca tcaagaaaat gtcttatagt ggaaagcagt ctactgagaa atggcaggat 300  
 attattaagg aagtcaagtt tctacaaaga ataaaacatc ccaacagtat agaatacaaa 360  
 ggctgttatt tacgtgaaca cacagcatgg cttgtaatgg aatattgttt aggatctgct 420  
 40 tcggatttac tagaagttca caaaaagcca ttacaagaag tggaaatagc agcaattaca 480  
 catggtgctc ttcagggatt agcctactta cattctcata ctatgattca tagagatatc 540  
 45 aaagcaggaa atatccttct gacagaacca ggccaggatga aacttgctga ctttggctct 600  
 gcttccatgg catcacctgc caattccttt gtgggaacgc cgtattggat ggccccagaa 660  
 gtaatttttag ccatggatga aggacaatat gatggcaaag tagatgtgtg gtctcttgga 720  
 50 ataacatgta ttgaactagc ggaaaggaag cctcctttat ttaatatgaa tgcaatgagt 780  
 gccttatatc acatagccca aaatgaatcc cctacactac agtctaata atggtctgat 840  
 55 tattttcgca actttgtaga ttcttgctc cagaaaatcc ctcaagatcg acctacatca 900  
 gaggaacttt taaagcacat atttgttctt cgggagcgcc ctgaaaccgt gttaatagat 960

5 ctcattcaga ggacaaagga tgcagtaaga gagctggaca atctgcagta tcgaaagatg 1020  
 aagaaactcc ttttccagga ggcacataat ggaccagcag tagaagcaca ggaagaagaa 1080  
 gaggaacaag atcatgggtgt tggccggaca ggaacagtta atagtgttgg aagtaatcaa 1140  
 tccattccca gcatgtccat cagtgccagc agccaaagca gtagtggttaa cagtcttcca 1200  
 10 gatgtctcag atgacaagag tgagctagac atgatggagg gagaccacac agtgatgtct 1260  
 aacagttctg ttatccattt aaaaccagag gaagaaaatt acagagaaga gggagatcct 1320  
 agaacaagag catcagatcc acaatctcca cccaagtat ctcgtcacia atcacactat 1380  
 15 cgtaatcgag aacactttgc tactatacgg acagcatcac tggttacgag gcaaatgcaa 1440  
 gaacatgagc aggactctga gcttagagaa caaatgtctg gctataagcg aatgaggcga 1500  
 20 caacatcaaa agcaactgat gactctggaa aacaagctaa aggctgagat ggatgaacat 1560  
 cgcttcagat tagacaaaga tcttgaaact cagcgtaca attttgctgc agaaatggag 1620  
 aaacttatca agaaacacca ggctgctatg gagaaagagg cttaaagtat gtccaatgaa 1680  
 25 gagaaaaaat ttcagcaaca tattcaggcc caacagaaga aagaactgaa tagttttctc 1740  
 gagtcccaga aaagagagta taaacttcga aaagagcagc ttaaagagga gctaaatgaa 1800  
 30 aaccagagta cccccaaaa agaaaaacag gagtggcttt caaagcagaa ggagaatata 1860  
 cagcatttcc aagcagaaga agaagctaac cttcttcgac gtcaaagaca atacctagag 1920  
 ctggaatgcc gtcgcttcaa gagaagaatg ttacttgggc gtcataactt agagcaggac 1980  
 35 cttgtcaggg aggagttaaa caaaagacag actcagaagg acttagagca tgccatgcta 2040  
 ctccgacagc atgaatctat gcaagaactg gagttccgcc acctcaacac aattcagaag 2100  
 40 atgcgctgtg agttgatcag attacagcat caaactgagc tcactaacca gctggaatat 2160  
 aataagcgaa gagaacgaga actaagacga aagcatgtca tggaagtctg acaacagcct 2220  
 aagagtttga agtctaaaga actccaaata aaaaagcagt ttcaggatac ctgcaaaatc 2280  
 45 caaaccagac agtaciaaagc attaagaaat cacctgctgg agactacacc aaagagttag 2340  
 caciaagctg ttctgaaacg gctcaaggag gaacagaccc ggaaattagc tatcttggct 2400  
 50 gagcagtatg atcacagcat taatgaaatg ctctccacac aagccctgcg tttggatgaa 2460  
 gcacaggaag cagagtcca ggttttgaag atgcagctgc agcaggaact ggagctgttg 2520  
 aatgcgtatc agagcaaaat caagatgcaa gctgaggcac aacatgatcg agagcttcgc 2580  
 55 gagcttgaac agagggtctc cctccggagg gcactcttag aacaaaagat tgaagaagag 2640

```

atgttggctt tgcagaatga gcgcacagaa cgaatacgaa gcctgttgga acgtcaagcc 2700
agagagattg aagcttttga ctctgaaagc atgagactag gtttttagtaa tatggtgctt 2760
5 tctaattctct cccctgaggc attcagccac agctacccgg gagcttctgg ttggtcacac 2820
aaccctactg ggggtccagg acctcactgg ggcatccca tgggtggccc accacaagct 2880
10 tggggccatc caatgcaagg tggaccccag ccatgggggtc acccttcagg gccaatgcaa 2940
ggggtacctc gaggtagcag tatgggagtc cgcaatagcc cccaagctct gaggcggaca 3000
gcttctgggg gacggacgga gcagggcatg agcagaagca cgagtgtcac ttcacaaata 3060
15 tccaatgggt cacacatgtc ttatacataa cttaataatt gagagtggca attccgctgg 3120
agctgtctgc caaaagaaac tgcctacaga catcatcaca gcagcctcct cacttgggta 3180
ctacagtgtg gaagctgagt gcatatggta tattttattc atttttgtaa agcgttctgt 3240
20 tttnggttta ctaattggga tgncatagta cttggctncc cgggt 3285

```

```

<210> 10
25 <211> 1005
<212> PRT
30 <213> Homo sapiens

```

```

<300>
35 <308> SpTREMBL
<309> 2000-10-01
<313> (1)..(1005)
40

```

```

<400> 10
45 Leu Leu Ser Arg Met Pro Ser Thr Asn Arg Ala Gly Ser Leu Lys Asp
1 5 10 15
Pro Glu Ile Ala Glu Leu Phe Phe Lys Glu Asp Pro Glu Lys Leu Phe
20 25 30
50 Thr Asp Leu Arg Glu Ile Gly His Gly Ser Phe Gly Ala Val Tyr Phe
35 40 45
Ala Arg Asp Val Arg Thr Asn Glu Val Val Ala Ile Lys Lys Met Ser
50 55 60
55 Tyr Ser Gly Lys Gln Ser Thr Glu Lys Trp Gln Asp Ile Ile Lys Glu
65 70 75 80

```

	Val	Lys	Phe	Leu	Gln	Arg	Ile	Lys	His	Pro	Asn	Ser	Ile	Glu	Tyr	Lys	
					85					90					95		
5	Gly	Cys	Tyr	Leu	Arg	Glu	His	Thr	Ala	Trp	Leu	Val	Met	Glu	Tyr	Cys	
				100					105					110			
	Leu	Gly	Ser	Ala	Ser	Asp	Leu	Leu	Glu	Val	His	Lys	Lys	Pro	Leu	Gln	
			115					120					125				
10	Glu	Val	Glu	Ile	Ala	Ala	Ile	Thr	His	Gly	Ala	Leu	Gln	Gly	Leu	Ala	
		130					135					140					
	Tyr	Leu	His	Ser	His	Thr	Met	Ile	His	Arg	Asp	Ile	Lys	Ala	Gly	Asn	
15	145					150				155						160	
	Ile	Leu	Leu	Thr	Glu	Pro	Gly	Gln	Val	Lys	Leu	Ala	Asp	Phe	Gly	Ser	
				165						170					175		
20	Ala	Ser	Met	Ala	Ser	Pro	Ala	Asn	Ser	Phe	Val	Gly	Thr	Pro	Tyr	Trp	
				180					185					190			
	Met	Ala	Pro	Glu	Val	Ile	Leu	Ala	Met	Asp	Glu	Gly	Gln	Tyr	Asp	Gly	
			195					200					205				
25	Lys	Val	Asp	Val	Trp	Ser	Leu	Gly	Ile	Thr	Cys	Ile	Glu	Leu	Ala	Glu	
		210					215					220					
	Arg	Lys	Pro	Pro	Leu	Phe	Asn	Met	Asn	Ala	Met	Ser	Ala	Leu	Tyr	His	
30	225					230				235						240	
	Ile	Ala	Gln	Asn	Glu	Ser	Pro	Thr	Leu	Gln	Ser	Asn	Glu	Trp	Ser	Asp	
				245						250					255		
35	Tyr	Phe	Arg	Asn	Phe	Val	Asp	Ser	Cys	Leu	Gln	Lys	Ile	Pro	Gln	Asp	
				260					265					270			
	Arg	Pro	Thr	Ser	Glu	Glu	Leu	Leu	Lys	His	Ile	Phe	Val	Leu	Arg	Glu	
			275					280					285				
40	Arg	Pro	Glu	Thr	Val	Leu	Ile	Asp	Leu	Ile	Gln	Arg	Thr	Lys	Asp	Ala	
		290					295					300					
	Val	Arg	Glu	Leu	Asp	Asn	Leu	Gln	Tyr	Arg	Lys	Met	Lys	Lys	Leu	Leu	
45	305					310				315						320	
	Phe	Gln	Glu	Ala	His	Asn	Gly	Pro	Ala	Val	Glu	Ala	Gln	Glu	Glu	Glu	
				325						330				335			
50	Glu	Glu	Gln	Asp	His	Gly	Val	Gly	Arg	Thr	Gly	Thr	Val	Asn	Ser	Val	
				340					345					350			
	Gly	Ser	Asn	Gln	Ser	Ile	Pro	Ser	Met	Ser	Ile	Ser	Ala	Ser	Ser	Gln	
			355					360					365				
55	Ser	Ser	Ser	Val	Asn	Ser	Leu	Pro	Asp	Val	Ser	Asp	Asp	Lys	Ser	Glu	
		370					375					380					

	Leu	Asp	Met	Met	Glu	Gly	Asp	His	Thr	Val	Met	Ser	Asn	Ser	Ser	Val	385	390	395	400
5	Ile	His	Leu	Lys	Pro	Glu	Glu	Glu	Asn	Tyr	Arg	Glu	Glu	Gly	Asp	Pro	405	410	415	
	Arg	Thr	Arg	Ala	Ser	Asp	Pro	Gln	Ser	Pro	Pro	Gln	Val	Ser	Arg	His	420	425	430	
10	Lys	Ser	His	Tyr	Arg	Asn	Arg	Glu	His	Phe	Ala	Thr	Ile	Arg	Thr	Ala	435	440	445	
	Ser	Leu	Val	Thr	Arg	Gln	Met	Gln	Glu	His	Glu	Gln	Asp	Ser	Glu	Leu	450	455	460	
15	Arg	Glu	Gln	Met	Ser	Gly	Tyr	Lys	Arg	Met	Arg	Arg	Gln	His	Gln	Lys	465	470	475	480
	Gln	Leu	Met	Thr	Leu	Glu	Asn	Lys	Leu	Lys	Ala	Glu	Met	Asp	Glu	His	485	490	495	
20	Arg	Leu	Arg	Leu	Asp	Lys	Asp	Leu	Glu	Thr	Gln	Arg	Asn	Asn	Phe	Ala	500	505	510	
25	Ala	Glu	Met	Glu	Lys	Leu	Ile	Lys	Lys	His	Gln	Ala	Ala	Met	Glu	Lys	515	520	525	
	Glu	Ala	Lys	Val	Met	Ser	Asn	Glu	Glu	Lys	Lys	Phe	Gln	Gln	His	Ile	530	535	540	
30	Gln	Ala	Gln	Gln	Lys	Lys	Glu	Leu	Asn	Ser	Phe	Leu	Glu	Ser	Gln	Lys	545	550	555	560
	Arg	Glu	Tyr	Lys	Leu	Arg	Lys	Glu	Gln	Leu	Lys	Glu	Glu	Leu	Asn	Glu	565	570	575	
35	Asn	Gln	Ser	Thr	Pro	Lys	Lys	Glu	Lys	Gln	Glu	Trp	Leu	Ser	Lys	Gln	580	585	590	
40	Lys	Glu	Asn	Ile	Gln	His	Phe	Gln	Ala	Glu	Glu	Glu	Ala	Asn	Leu	Leu	595	600	605	
	Arg	Arg	Gln	Arg	Gln	Tyr	Leu	Glu	Leu	Glu	Cys	Arg	Arg	Phe	Lys	Arg	610	615	620	
45	Arg	Met	Leu	Leu	Gly	Arg	His	Asn	Leu	Glu	Gln	Asp	Leu	Val	Arg	Glu	625	630	635	640
	Glu	Leu	Asn	Lys	Arg	Gln	Thr	Gln	Lys	Asp	Leu	Glu	His	Ala	Met	Leu	645	650	655	
50	Leu	Arg	Gln	His	Glu	Ser	Met	Gln	Glu	Leu	Glu	Phe	Arg	His	Leu	Asn	660	665	670	
55	Thr	Ile	Gln	Lys	Met	Arg	Cys	Glu	Leu	Ile	Arg	Leu	Gln	His	Gln	Thr	675	680	685	



	Glu	Leu	Thr	Asn	Gln	Leu	Glu	Tyr	Asn	Lys	Arg	Arg	Glu	Arg	Glu	Leu
	690						695					700				
5	Arg	Arg	Lys	His	Val	Met	Glu	Val	Arg	Gln	Gln	Pro	Lys	Ser	Leu	Lys
	705					710					715					720
	Ser	Lys	Glu	Leu	Gln	Ile	Lys	Lys	Gln	Phe	Gln	Asp	Thr	Cys	Lys	Ile
					725					730					735	
10	Gln	Thr	Arg	Gln	Tyr	Lys	Ala	Leu	Arg	Asn	His	Leu	Leu	Glu	Thr	Thr
				740					745					750		
	Pro	Lys	Ser	Glu	His	Lys	Ala	Val	Leu	Lys	Arg	Leu	Lys	Glu	Glu	Gln
15			755					760					765			
	Thr	Arg	Lys	Leu	Ala	Ile	Leu	Ala	Glu	Gln	Tyr	Asp	His	Ser	Ile	Asn
	770						775					780				
20	Glu	Met	Leu	Ser	Thr	Gln	Ala	Leu	Arg	Leu	Asp	Glu	Ala	Gln	Glu	Ala
	785					790					795					800
	Glu	Cys	Gln	Val	Leu	Lys	Met	Gln	Leu	Gln	Gln	Glu	Leu	Glu	Leu	Leu
					805					810					815	
25	Asn	Ala	Tyr	Gln	Ser	Lys	Ile	Lys	Met	Gln	Ala	Glu	Ala	Gln	His	Asp
				820					825					830		
	Arg	Glu	Leu	Arg	Glu	Leu	Glu	Gln	Arg	Val	Ser	Leu	Arg	Arg	Ala	Leu
30			835					840					845			
	Leu	Glu	Gln	Lys	Ile	Glu	Glu	Glu	Met	Leu	Ala	Leu	Gln	Asn	Glu	Arg
	850						855					860				
35	Thr	Glu	Arg	Ile	Arg	Ser	Leu	Leu	Glu	Arg	Gln	Ala	Arg	Glu	Ile	Glu
	865					870					875					880
	Ala	Phe	Asp	Ser	Glu	Ser	Met	Arg	Leu	Gly	Phe	Ser	Asn	Met	Val	Leu
					885					890					895	
40	Ser	Asn	Leu	Ser	Pro	Glu	Ala	Phe	Ser	His	Ser	Tyr	Pro	Gly	Ala	Ser
				900					905					910		
	Gly	Trp	Ser	His	Asn	Pro	Thr	Gly	Gly	Pro	Gly	Pro	His	Trp	Gly	His
45			915					920					925			
	Pro	Met	Gly	Gly	Pro	Pro	Gln	Ala	Trp	Gly	His	Pro	Met	Gln	Gly	Gly
	930						935					940				
50	Pro	Gln	Pro	Trp	Gly	His	Pro	Ser	Gly	Pro	Met	Gln	Gly	Val	Pro	Arg
	945					950					955					960
	Gly	Ser	Ser	Met	Gly	Val	Arg	Asn	Ser	Pro	Gln	Ala	Leu	Arg	Arg	Thr
					965					970					975	
55	Ala	Ser	Gly	Gly	Arg	Thr	Glu	Gln	Gly	Met	Ser	Arg	Ser	Thr	Ser	Val
				980					985					990		

Thr Ser Gln Ile Ser Asn Gly Ser His Met Ser Tyr Thr  
 995 1000 1005

5  
 <210> 11  
 <211> 1576  
 10 <212> DNA  
 <213> artificial sequence  
 15 <220>  
 <223> RNAi fragment T17E9.1a (kin-18)  
 <400> 11  
 20 cgaaaaccag cagaagagcg aatgtcagct gaagaatgct ttcgacatcc attcattcaa 60  
 cggctctcgcc catcagacac aattcaggaa ctcatcaga gaacgaaaaa tatggtatta 120  
 gagttggata attttcaata caaaaagatg agaaaactca tgtatttgga tgaaacagaa 180  
 25 ggaaaagaag gaagtgaagg aaatggagca tctgatgatt tagattttca tggaaatgaa 240  
 gctaattcaa ttggaagagg tagtttttaa aattcaaagt gaaaatatta atatcttgga 300  
 30 ataattttta taatattgct ttaaaccctc agcttttttt tgcagactct atcccttagt 360  
 tgttcgtttt ccattctatc tcgttttcag caggagattc tgcgtcatct cgaagtgcct 420  
 ctcttacttc tttccgatca atgcagagta gtggaggagc tgggtctttta gtgtccacca 480  
 35 atacgacggg tgctatggat aatgtgcatg gtactgtact gttttttttg ttttaggaat 540  
 ggctttatta tttcctgcaa agttcaaaaa ttccatttat tttagttttt ctctcgaaat 600  
 40 tcatcgcgca acattgagaa tctttcaaaa ttttcaggat cctctggata cggtaatgga 660  
 agtagttcga cgacgagctc cgcacgccgc cgtcctccaa ttccttcgca aatgctctct 720  
 tctacatcaa cgtctggtgt tggaactatg ccgagtcatt gatcagttgg agcatcgatt 780  
 45 acggcgatcg cagtcaatcc aacaccgtct ccttcagaac ctatcccaac atcacaacca 840  
 acatcgaaat cagaatcatc ttctatactc gaaactgcac acgatgatcc tttggacacg 900  
 50 tcgatacgtg ctccagtgaag agacttgcatt atgccgcatt gagcagtcaa ggaacgaata 960  
 gccacgttgc aaaatcacia attcgcgacg cttcgttccc agagaataat caatcaggaa 1020  
 caagaagaat atacgaaaga gaacaatatg tatgagcaaaa tgagcaagta caagcatcta 1080  
 55 cgacaagcac atcaciaaaga gctccaacia tttgaagaac gatgtgcatt agatagagag 1140

caactgctg tgaaaatgga tcgagaactc gaacaattga caacgacata ctcgaaagaa 1200  
aagatgagag tgaggtgttc acagaataat gaactagaca aacggaaaaa agatatcgaa 1260  
5 gatggggaga aaaagatgaa aaagacgaaa aatagtcaaa atcagcagca gatgaaactg 1320  
tattcagcgc aacaattgaa agaatacaag tataacaagg aggcacagaa aacagtgaga 1380  
attcactttt atttgatttc tgtaaagaaa ttatacgaaa tttagacttt ataaattttt 1440  
10 aaatatgaaa gttctggtca ctttttcagc tgcttctcca cttttttcaa agtttattat 1500  
ttagtcttga ataatttttt aaaaaatgtc ctaaaccaag aattttcagc gattacgaag 1560  
15 tctgaacatg cctcga 1576

<210> 12

20 <211> 20

<212> DNA

25 <213> artificial sequence

<220>

30 <223> primer

<400> 12

cgaaaaccag cagaagagcg 20

35 <210> 13

<211> 21

<212> DNA

40 <213> artificial sequence

<220>

45 <223> primer

<400> 13

50 tcgaggcatg ttcagacttc g 21